

AMENDMENTS TO THE CLAIMS

Please replace the claims with the following amendments:

1-67. (cancelled).

68. (New) A plant comprising a transgenic rootstock resistant to a viral disease other than by means of expression of an anti-viral protein and a scion susceptible to the viral disease, wherein the engrafted plant is resistant to said viral disease.

69. (New) The plant according to claim 68, wherein the transgenic rootstock resistant to a viral disease comprises a nucleic acid sequence having at least 90% identity to at least one segment of the viral genome.

70. (New) The plant according to claim 69, wherein the transgenic rootstock resistant to a viral disease comprises a DNA construct designed for generating siRNAs targeted to the at least one segment of the viral genome.

71. (New) The plant according to claim 69, wherein the at least one segment of the viral genome encodes a viral protein or parts thereof, selected from the group consisting of a viral coat protein, a viral replication protein, a viral movement protein or parts thereof.

72. (New) The plant according to claim 71, wherein the viral protein is a viral replication protein or part thereof.

73. (New) The plant according to claim 72, wherein the transgenic rootstock is resistant to a disease caused by a soil-borne virus, and wherein said plant is protected from a disease caused by a soil-borne virus selected from the group consisting of nematode-transmitted viruses: Nepoviruses: Arabis mosaic virus, Grapevine fanleaf virus, Tomato black ring virus, Raspberry ringspot virus, Tomato ringspot virus, and Tobacco ringspot virus; Tobraviruses: Pea early browning virus, Tobacco rattle virus and Pepper ringspot virus; fungal-transmitted viruses: Cucumber leafspot virus, Cucumber necrosis virus, Melon necrotic spot virus, Red clover necrotic mosaic virus, Squash necrosis virus, Tobacco necrosis satellite virus, Lettuce big-vein virus, Pepper yellow vein virus, Beet

necrotic yellow vein virus, Beet soil-borne virus, Oat golden stripe virus, Peanut clump virus, Potato mop top virus, Rice stripe necrosis virus, Soil-borne wheat mosaic virus, Barley mild mosaic virus, Barley yellow mosaic virus, Oat mosaic virus, Rice necrosis mosaic virus, Wheat spindle streak mosaic virus and Wheat yellow mosaic virus; viruses transmitted via root wound: Tobamovirus genera: Tobacco mosaic virus, Tomato mosaic virus, Cucumber green mottle mosaic tobamovirus, Cucumber fruit mottle mosaic virus, Kyuri green mottle mosaic virus, Odontoglossum ringspot virus, Paprika mild mottle virus, Pepper mild mottle virus, Ribgrass mosaic virus and Tobacco mild green mosaic virus; and viruses transmitted by unknown rout: Watercress yellow spot virus, Broad been necrotic wilt virus, Peach rosette mosaic virus and Sugarcane chlorotic streak virus.

74. (New) The plant according to claim 71, wherein the at least one segment of the viral genome encodes a putative 54 kDa protein being a fragment of the replication protein of cucumber fruit mottle mosaic virus (CFMMV).

75. (New) The plant according to claim 74, wherein the at least one segment of the viral genome encoding a putative 54 kDa protein has the sequence set forth in SEQ ID NO:1.

76. (New) The plant according to claim 75, wherein the plant is protected from a disease caused by a soil-borne virus of the tobamovirus genus.

77. (New) The plant according to claim 76, wherein the plant is protected from a disease caused by CFMMV.

78. (New) The plant according to claim 77, wherein the plant is of the *Cucurbitaceae* family.

79. (New) The plant according to claim 78, wherein the plant is a cucumber plant.

80. (New) The plant according to claim 70, wherein the DNA construct comprises nucleic acid sequence encoding an RNA sequence that forms at least one double-stranded RNA molecule, wherein the double stranded RNA molecule mediates cleavage of the at least one segment of the viral genome.

81. (New) The plant according to claim 80, wherein the DNA construct comprises:

- a. at least one plant expressible promoter operably linked to;
- b. a nucleic acid sequence encoding an RNA sequence that forms at least one double stranded RNA, wherein the double stranded RNA molecule comprises a first nucleotide sequence of at least 20 contiguous nucleotides having at least 90% sequence identity to the sense nucleotide sequence of the target segment of the viral genome and a second nucleotide sequence of at least 20 contiguous nucleotides having at least 90% sequence identity to the complementary sequence of the sense nucleotide sequence of said target segment of said viral genome; and optionally
- c. a transcription termination signal.

82. (New) The plant according to claim 81, wherein the first and the second nucleotide sequences are separated by a spacer sequence.

83. (New) The plant according to claim 82, wherein the spacer sequence comprises a sequence of an intron.

84. (New) The plant according to claim 83, wherein the spacer sequence comprises an intron of the castor bean catalase gene, having the sequence set forth in SEQ ID NO:3.

85. (New) The plant according to claim 81, wherein the DNA construct comprises the first and the second nucleotide sequences operably linked to the same promoter.

86. (New) The plant according to claim 80, wherein the plant is resistant to a virus selected from the group consisting of a soil-borne virus and a virus transmitted by a vector affecting the aerial part of the plant.

87. (New) The plant according to claim 86, wherein the soil-borne virus is selected from the group consisting of nematode-transmitted viruses: Nepoviruses: Arabis

mosaic virus, Grapevine fanleaf virus, Tomato black ring virus, Raspberry ringspot virus, Tomato ringspot virus, and Tobacco ringspot virus; Tobraviruses: Pea early browning virus, Tobacco rattle virus and Pepper ringspot virus; fungal-transmitted viruses: Cucumber leafspot virus, Cucumber necrosis virus, Melon necrotic spot virus, Red clover necrotic mosaic virus, Squash necrosis virus, Tobacco necrosis satellite virus, Lettuce big-vein virus, Pepper yellow vein virus, Beet necrotic yellow vein virus, Beet soil-borne virus, Oat golden stripe virus, Peanut clump virus, Potato mop top virus, Rice stripe necrosis virus, Soil-borne wheat mosaic virus, Barley mild mosaic virus, Barley yellow mosaic virus, Oat mosaic virus, Rice necrosis mosaic virus, Wheat spindle streak mosaic virus and Wheat yellow mosaic virus; viruses transmitted via root wound: Tobamovirus genera: Tobacco mosaic virus, Tomato mosaic virus, Cucumber green mottle mosaic tobamovirus, Cucumber fruit mottle mosaic virus, Kyuri green mottle mosaic virus, Odontoglossum ringspot virus, Paprika mild mottle virus, Pepper mild mottle virus, Ribgrass mosaic virus and Tobacco mild green mosaic virus; and viruses transmitted by unknown rout: Watercress yellow spot virus, Broad been necrotic wilt virus, Peach rosette mosaic virus and Sugarcane chlorotic streak virus.

88. (New) The plant according to claim 86, wherein the virus transmitted by a vector affecting the aerial parts of the plant is of a family selected from the group consisting of: *Caulimoviridae*, *Geminiviridae*, *Circoviridae*, *Reoviridae*, *Tartitiviridae*, *Bromoviridae*, *Comoviridae*, *Potyviridae*, *Tombusviridae*, *Sequiviridae*, *Clostriviridae* and *Luteoviridae*; *Tobamovirus*, *Tobravirus*, *Potexvirus*, *Carlavirus*, *Allexivirus*, *Capillovirus*, *Foveavirus*, *Trichovirus*, *Vitivirus*, *Furovirus*, *Pecluvirus*, *Pomovirus*, *Benyvirus*, *Hordeivirus*, *Sobemovirus*, *Marafivirus*, *Tymovirus*, *Idaeovirus*, *Ourmivirus*, *Umbravirus*.

89. (New) The plant according to claim 80, wherein the at least one segment of the viral genome comprises the 3' end of Zucchini Yellow Mosaic Virus (ZYMV) genome.

90. (New) The plant according to claim 89, wherein the at least one segment of the viral genome comprises the nucleic acid sequence set forth in SEQ ID NO:2.

91. (New) The plant according to claim 81, wherein the first nucleotide sequence comprises a nucleic acid sequence having at least 90% identity to the nucleotide sequence set forth in SEQ ID NO:2 or fragments thereof.

92. (New) The plant according to claim 91, wherein the second nucleotide sequence comprises a nucleic acid sequence having at least 90% identity to the complement of the nucleotide sequence set forth in SEQ ID NO:2 or fragments thereof.

93. (New) The plant according to claim 92, wherein the plant is resistant to a disease caused by a virus from the *Potyviridae* family.

94. (New) The plant according to claim 93, wherein the plant is resistant to ZYMV.

95. (New) The plant according to claim 69, wherein the nucleic acid sequence further comprises at least one expression control sequence, selected from the group consisting of a promoter, an enhancer, a transcription factor, a splicing signal, and a termination sequence.

96. (New) The plant according to claim 95, wherein the promoter is a constitutive promoter.

97. (New) The plant according to claim 69, wherein the nucleic acid sequence further comprises a selectable marker.

98. (New) The plant according to claim 97, wherein the selectable marker is selected from a polynucleotide sequence encoding a product conferring antibiotic resistance and a reporter gene encoding a detectable product.

99. (New) The plant according to claim 95, wherein the transcription termination signal is the NOS terminator.

100. (New) A method for producing a plant resistant to a viral disease comprising:

- a. providing a transgenic rootstock resistant to the viral disease other than by means of expression of an anti-viral protein;

- b. providing a scion susceptible to said viral disease; and
 - c. grafting the scion onto the rootstock;
- thereby obtaining an engrafted plant resistant to the viral disease.

101. (New) The method according to claim 100, wherein the rootstock is transformed with a nucleic acid sequence having at least 90% identity to at least one segment of the viral genome as to produce a transgenic rootstock resistant to the viral disease.

102. (New) The method according to claim 101, wherein the rootstock is transformed with a DNA construct designed for generating siRNAs targeted to the at least one segment of the viral genome.

103. (New) The method according to claim 101, wherein the at least one segment of the viral genome encodes a viral protein or parts thereof, selected from the group consisting of a viral coat protein, a viral replication protein, a viral movement protein or parts thereof.

104. (New) The method according to claim 103, wherein the viral protein is a viral replication protein or part thereof.

105. (New) The method according to claim 104, wherein the transgenic rootstock is resistant to a disease caused by a soil-borne virus, and wherein said plant is protected from a disease caused by a soil-borne virus selected from the group consisting of nematode-transmitted viruses: Nepoviruses: Arabis mosaic virus, Grapevine fanleaf virus, Tomato black ring virus, Raspberry ringspot virus, Tomato ringspot virus, and Tobacco ringspot virus; Tobraviruses: Pea early browning virus, Tobacco rattle virus and Pepper ringspot virus; fungal-transmitted viruses: Cucumber leafspot virus, Cucumber necrosis virus, Melon necrotic spot virus, Red clover necrotic mosaic virus, Squash necrosis virus, Tobacco necrosis satellite virus, Lettuce big-vein virus, Pepper yellow vein virus, Beet necrotic yellow vein virus, Beet soil-borne virus, Oat golden stripe virus, Peanut clump virus, Potato mop top virus, Rice stripe necrosis virus, Soil-borne wheat mosaic virus, Barley mild mosaic virus, Barley yellow mosaic virus, Oat mosaic virus, Rice necrosis mosaic virus, Wheat spindle streak mosaic virus and Wheat yellow mosaic virus; viruses

transmitted via root wound: Tobamovirus genera: Tobacco mosaic virus, Tomato mosaic virus, Cucumber green mottle mosaic tobamovirus, Cucumber fruit mottle mosaic virus, Kyuri green mottle mosaic virus, Odontoglossum ringspot virus, Paprika mild mottle virus, Pepper mild mottle virus, Ribgrass mosaic virus and Tobacco mild green mosaic virus; and viruses transmitted by unknown rout: Watercress yellow spot virus, Broad been necrotic wilt virus, Peach rosette mosaic virus and Sugarcane chlorotic streak virus.

106. (New) The method according to claim 103, wherein the transgenic rootstock comprises a nucleic acid sequence encoding a putative 54 kDa protein being a fragment of the replication protein of cucumber fruit mottle mosaic virus (CFMMV).

107. (New) The method according to claim 106, wherein the transgenic rootstock comprises a nucleic acid sequence encoding a putative 54 kDa protein having the sequence set forth in SEQ ID NO:1.

108. (New) The method according to claim 107, wherein the plant is protected from a disease caused by a soil-borne virus of the tobamovirus genus.

109. (New) The method according to claim 108, wherein the plant is protected from a disease caused by CFMMV.

110. (New) The method according to claim 109, wherein the plant is of the *Cucurbitaceae* family.

111. (New) The method according to 110, wherein the plant is a cucumber plant.

112. (New) The method according to claim 102, wherein the DNA construct comprises nucleic acid sequence encoding an RNA sequence that forms at least one double-stranded RNA molecule, wherein the double stranded RNA molecule mediates cleavage of the at least one segment of the viral genome.

113. (New) The method according to claim 112, wherein the DNA construct comprises:

- a. at least one plant expressible promoter operably linked to;

- b. a nucleic acid sequence encoding an RNA sequence that forms at least one double stranded RNA, wherein the double stranded RNA molecule comprises a first nucleotide sequence of at least 20 contiguous nucleotides having at least 90% sequence identity to the sense nucleotide sequence of the target segment of the viral genome and a second nucleotide sequence of at least 20 contiguous nucleotides having at least 90% sequence identity to the complementary sequence of the sense nucleotide sequence of said target segment of said viral genome; and optionally
- c. a transcription termination signal.

114. (New) The method according to claim 113, wherein the first and the second nucleotide sequences are separated by a spacer sequence.

115. (New) The method according to claim 114, wherein the spacer sequence comprises a sequence of an intron.

116. (New) The method according to claim 115, wherein the spacer sequence comprises an intron of the castor bean catalase gene, having the sequence set forth in SEQ ID NO:3.

117. (New) The method according to claim 113, wherein the DNA construct comprises the first and the second nucleotide sequences operably linked to the same promoter.

118. (New) The method according to claim 102, wherein the plant is resistant to a virus selected from the group consisting of a soil-borne virus and a virus transmitted by a vector affecting the aerial part of the plant.

119. (New) The method according to claim 118, wherein the soil-borne virus is selected from the group consisting of nematode-transmitted viruses: Nepoviruses: Arabis mosaic virus, Grapevine fanleaf virus, Tomato black ring virus, Raspberry ringspot virus, Tomato ringspot virus, and Tobacco ringspot virus; Tobraviruses: Pea early browning virus, Tobacco rattle virus and Pepper ringspot virus; fungal-transmitted viruses:

Cucumber leafspot virus, Cucumber necrosis virus, Melon necrotic spot virus, Red clover necrotic mosaic virus, Squash necrosis virus, Tobacco necrosis satellite virus, Lettuce big-vein virus, Pepper yellow vein virus, Beet necrotic yellow vein virus, Beet soil-borne virus, Oat golden stripe virus, Peanut clump virus, Potato mop top virus, Rice stripe necrosis virus, Soil-borne wheat mosaic virus, Barley mild mosaic virus, Barley yellow mosaic virus, Oat mosaic virus, Rice necrosis mosaic virus, Wheat spindle streak mosaic virus and Wheat yellow mosaic virus; viruses transmitted via root wound: Tobamovirus genera: Tobacco mosaic virus, Tomato mosaic virus, Cucumber green mottle mosaic tobamovirus, Cucumber fruit mottle mosaic virus, Kyuri green mottle mosaic virus, Odontoglossum ringspot virus, Paprika mild mottle virus, Pepper mild mottle virus, Ribgrass mosaic virus and Tobacco mild green mosaic virus; and viruses transmitted by unknown rout: Watercress yellow spot virus, Broad been necrotic wilt virus, Peach rosette mosaic virus and Sugarcane chlorotic streak virus.

120. (New) The method according to claim 118, wherein the virus transmitted by a vector affecting the aerial parts of the plant is of a family selected from the group consisting of: *Caulimoviridae*, *Geminiviridae*, *Circoviridae*, *Reoviridae*, *Tartitviridae*, *Bromoviridae*, *Comoviridae*, *Potyviridae*, *Tombusviridae*, *Sequiviridae*, *Clostraviridae* and *Luteoviridae*; *Tobamovirus*, *Tobravirus*, *Potexvirus*, *Carlavirus*, *Allexivirus*, *Capillovirus*, *Foveavirus*, *Trichovirus*, *Vitivirus*, *Furovirus*, *Pecluvirus*, *Pomovirus*, *Benyvirus*, *Hordeivirus*, *Sobemovirus*, *Marafivirus*, *Tymovirus*, *Idaeovirus*, *Ourmivirus*, *Umbravirus*.

121. (New) The method according to claim 112, wherein the at least one segment of the viral genome comprises the 3' end of Zucchini Yellow Mosaic Virus (ZYMV) genome.

122. (New) The method according to claim 121, wherein the at least one segment of the viral genome comprises the nucleic acid sequence set forth in SEQ ID NO:2.

123. (New) The method according to claim 113, wherein the first nucleotide sequence comprises a nucleic acid sequence having at least 90% identity to the nucleotide sequence set forth in SEQ ID NO:2 or fragments thereof.

124. (New) The method according to claim 123, wherein the second nucleotide sequence comprises a nucleic acid sequence having at least 90% identity to the complement of the nucleotide sequence set forth in SEQ ID NO:2 or fragments thereof.

125. (New) The method according to claim 124, wherein the plant is resistant to a disease caused by a virus from the *Potyviridae* family.

126. (New) The method according to claim 125, wherein the plant is resistant to ZYMV.

127. (New) An engrafted plant produced by the method of claim 100.

128. (New) The plant according to claim 127, wherein the plant is resistant to a virus selected from the group consisting of a soil-borne virus and a virus transmitted by a vector affecting the aerial part of the plant.

129. (New) The plant according to claim 128, wherein the plant is resistant to a soil-borne virus selected from the group consisting of nematode-transmitted viruses: Nepoviruses: Arabis mosaic virus, Grapevine fanleaf virus, Tomato black ring virus, Raspberry ringspot virus, Tomato ringspot virus, and Tobacco ringspot virus; Tobraviruses: Pea early browning virus, Tobacco rattle virus and Pepper ringspot virus; fungal-transmitted viruses: Cucumber leafspot virus, Cucumber necrosis virus, Melon necrotic spot virus, Red clover necrotic mosaic virus, Squash necrosis virus, Tobacco necrosis satellite virus, Lettuce big-vein virus, Pepper yellow vein virus, Beet necrotic yellow vein virus, Beet soil-borne virus, Oat golden stripe virus, Peanut clump virus, Potato mop top virus, Rice stripe necrosis virus, Soil-borne wheat mosaic virus, Barley mild mosaic virus, Barley yellow mosaic virus, Oat mosaic virus, Rice necrosis mosaic virus, Wheat spindle streak mosaic virus and Wheat yellow mosaic virus; viruses transmitted via root wound: Tobamovirus genera: Tobacco mosaic virus, Tomato mosaic virus, Cucumber green mottle mosaic tobamovirus, Cucumber fruit mottle mosaic virus,

Kyuri green mottle mosaic virus, Odontoglossum ringspot virus, Paprika mild mottle virus, Pepper mild mottle virus, Ribgrass mosaic virus and Tobacco mild green mosaic virus; and viruses transmitted by unknown rout: Watercress yellow spot virus, Broad been necrotic wilt virus, Peach rosette mosaic virus and Sugarcane chlorotic streak virus.

130. (New) The plant according to claim 128, wherein the plant is resistant to a virus transmitted by a vector affecting the aerial parts of the plant of a family selected from the group consisting of: *Caulimoviridae*, *Geminiviridae*, *Circoviridae*, *Reoviridae*, *Tartitiviridae*, *Bromoviridae*, *Comoviridae*, *Potyviridae*, *Tombusviridae*, *Sequiviridae*, *Clostriviridae* and *Luteoviridae*; *Tobamovirus*, *Tobravirus*, *Potexvirus*, *Carlavirus*, *Allexivirus*, *Capillovirus*, *Foveavirus*, *Trichovirus*, *Vitivirus*, *Furovirus*, *Pecluvirus*, *Pomovirus*, *Benyvirus*, *Hordeivirus*, *Sobemovirus*, *Marafivirus*, *Tymovirus*, *Idaeovirus*, *Ourmivirus*, *Umbravirus*.